

TABLE 1

SEQ ID	Sequence Calling Assembly	Base pos. of SNP	Polymorphic Sequence	Base before gap (1)	Amino Acid before	Amino Acid after	Type of Change	Protein classification of CuratGen kinase receptor	Name of protein identified following a BLASTX analysis of the CuratGen sequence	P value	Allele Freq. (p.e.)	Map Location	Therapeutic Area #1	Therapeutic Area #2
1, 2	cg44928667	1090	TGGAGCAGAAAGG TGAGCTGGACT CCAGG(gap)TATC TGAGTGTCTCGC TGAAGAAATACC AGACTGAGCAA GGAG	TATCT GAGT G(2)	Arg	Lys	Frameshift	Human Gene SPTRMBL1-ID Q60437 INSULIN RECEPTOR TYROSINE KINASE 53 KDA SUBSTRATE - UNKNOWN, 521 aa	4.60E-246	10bp in 3 of 11	17	Metabolic/endocrine/cardiovascular	Metabolic/endocrine/cardiovascular	
3, 4	cg43957213	1529	CATACATAACG GGCAAGATTCAG TCCCTGACCGCA -AAGTGCGCA- CTTACAGCTCTAG TGGGAAGGGAG ACACAAAT	gap (3)	G (4)		Silent, Non-Coding	Human Gene SWISSPROT-ID P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa [pols SWISSPROT-ID P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa [pols TREMBLNEW-ID E308262 AMILORIDE-SENSITIVE EPITHELIAL SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 669 aa	good 10 of 1p36 1 20		Renal Disease	Metabolic/endocrine/cardiovascular		
5, 6	cg44912878	1164	ACCCCATCATGG AGGTCTGATG TCICATCAC CACTGCCAG CCACC	T (5)	C (6)	Ala	Val	CONSERVATIVE	Human Gene SWISSPROT-ID P17538-6 PHOSPHORFRUCTOKINASE, LIVER TYPE (EC 2.7.1.11) (PHOSPHORFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (PHOSPHORFRUCTO-KINASE ISOZYME B) - HOMO SAPIENS (HUMAN), 780 aa	good 2 of 21 9		Metabolic/endocrine/cardiovascular		

TABLE 1
Effect of $\text{Na}_2\text{S}_2\text{O}_5$ on the Polymerization of $\text{CH}_2=\text{CH}-\text{CH}_2\text{Cl}$ in the Presence of FeCl_3

Sequence Calling Assembly ID	Base pos. of SNP	Polymorphic Sequence	Base before	Base after	Amino Acid before	Amino Acid after	Type of Change	Protein classification of Curagen gene	Name of protein identified following a BLASTX analysis of the Curagen sequence	p value	Allele freq. (pred.)	Map Location	Therapeutic Area #1	Therapeutic Area #2
SEQ ID: 7, 8	cg44912878	CT-A- TCCTGGCACCC TG-CCAGGCC CCTG/C/GCTG TGCTT-GAG- CCA-GCCTG- CCAGGCC	G (7)	C (8)			3' UTR	kinase	Human Gene SWISSPROT-ID P17838-6 PHOSPHOFRUCTOKINASE, LIVER TYPE (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTO-1-KINASE ISOZYME B) - HOMO SAPIENS (HUMAN), 780 aa	good 7 of 20	21	Metabolic/endocrine/cardiovascular		
9, 10	cg44912878	ATCATCCAGCTG GGGGCACTTC ATTGGCAGCGCT GGCTTCG/GC GCCCTTACACC AGGGAGGGCG CCGGCAGCGG	CG (9)	GC (10)	Cys	Ser	CONSERVATIVE	kinase	Human Gene SWISSPROT-ID P17838-6 PHOSPHOFRUCTOKINASE, LIVER TYPE (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTO-1-KINASE ISOZYME B) - HOMO SAPIENS (HUMAN), 780 aa	good 4 of 8	21	Metabolic/endocrine/cardiovascular		
11, 12	cg44921974	TGAGAGCTGGTC ACAGACTGTGAT TTTT-GA- AAGCTTGTAC CAGTTTATGTCA CCCTCAAACTGA ACCACGTCTTG	C (11)	T (12)	Thr	Ala	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SWISSPROT- AC P07148 FATTY ACID-BINDING PROTEIN, LIVER (L-FABP) - Homo sapiens (Human), 127 aa	1.30E-06	9 of 30	2 (4q28)	Metabolic/endocrine/cardiovascular	
13, 14	95124747													Metabolic/endocrine/cardiovascular

TABLE 1

SEQ ID	Sequence Calling Assembly	Base pos. of SNP	Base pos. of Polymorphic Sequence	Base before	Base after	Amino Acid before	Amino Acid after	Type of Change	Protein classification of CurateGen gene	Name of protein identified following a BLASTX analysis of the CurateGen sequence	p value	Allele Freq. (pred.)	Map Location	Therapeutic Area #1	Therapeutic Area #2
15, 16	88073933	751	GAGATGGGCGCTA	A (15)	G (16)	Ile	Val	Conservative	CurateGen gene	Carbonic Anhydrase 3		5 of 12	8	Metabolic/endocrine/cardiovascular	Metabolic/endocrine/cardiovascular
17, 18	cg43953338	1246	AATTTGGG-TGGT- TTGAAGGATCAC ATAAA- GGAGATCCAGA A/GIA-TGCC- GGGGTTGATCT -TATIGCTT	A (17)	G (18)			Silent-Coding	synthase	Human Gene Homologous to SWISSPROT-ID P44708 GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (EC 2.6.1.6) (HEXOSEPHOSPHATE D-AMINOTRANSFERASE) (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT) (L-GLUTAMINE-D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GLUCOSAMINE-6-PHOSPHATE SYNTHASE) - HAEMOPHILUS INFLUENZAE, 609 aa	3.10E-107	4 of 40	2 (2p13)	Metabolic/endocrine/cardiovascular	Metabolic/endocrine/cardiovascular
19, 20	cg43953338	3084	ATGTTGGGTATC	G (19)	T (20)			3' UTR	synthase	Human Gene Homologous to SWISSPROT-ID P44708 GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (EC 2.6.1.6) (HEXOSEPHOSPHATE D-AMINOTRANSFERASE) (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT) (L-GLUTAMINE-D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GLUCOSAMINE-6-PHOSPHATE SYNTHASE) - HAEMOPHILUS INFLUENZAE, 609 aa	3.10E-107	4 of 10	2 (2p13)	Metabolic/endocrine/cardiovascular	Metabolic/endocrine/cardiovascular

TABLE 1. *Estimated Number of Cases of Measles in the United States, 1960-1964*

Sequence Calling Assembly SEQ ID	Base pos. of SNP	Base before	Base after	Amino Acid before	Amino Acid after	Type of Change	Protein classification of Curagen gene	Name of protein identified following a BLASTX analysis of the Curagen sequence	p value	Allele Freq. (pred.)	Map Location	Therapeutic Area #1	Therapeutic Area #2
21, 22 cg42930646	1229	TCICAGGCCAC AAATAGGAGTCG TCATGTACTG ATGGGGATAGCG TA- TGGATGAA[AG TGGGAGATAG GAGGACCTGCT TCTGCTGAGGA CTGGAGG	A (21) G (22)	Met		NON-CONSERVATIVE	lummun	Human Gene SWISS-PROT-ID P07221 CALSEQUSTRIN, SKELETAL MUSCLE ISOFORM PRECURSOR (ASPARTACTIN) (LAMININ-BINDING PROTEIN)-ORYCTOLAGUS CUNICULUS (RABBIT), 395 aa	1.80E-198	4 of 19	1	Metabolic/endocrine/cardiovascular	Bone Disease
23, 24 94842816	1303	CCGAGTTCCT CTTCCCAGACT CAGAGCCCCACTT ATTTTCACATCT TTCGAAACTCCG ACCGGACATCCA ACCGAGCGGGTT CAGC	A (23)	T (24)	Asn	Lys	NON-CONSERVATIVE	Secreted hormone	Adrenomedullin	4 of 55	11	Metabolic/endocrine/cardiovascular	
25, 26 88048627	3294	CCTATTACAGA GAGGATCGAGCA TGTTCCCTCTTC C/C/TCTCCACCT GTTGATCCCTCG ATCTCTTCCTCA TCTTCCCTGATAGT GGGGATGA	C (25)	T (26)	Pro	Ser	NON-CONSERVATIVE	Membrane protein	Prion protein (new variant)	2 of 16	20p12.1-13	Metabolic/endocrine/cardiovascular	CNS Disorders
27, 28 88048627	2968	GTTGCTGAGCA CTGGGGCACTG GTTGGGGGGCCTT GGCGCGCTA- CAGTGTGCTGGGA AGTGCCCATGAGC AGGGCCATCATCA CATT	A (27)	G (28)	Silent-Coding	Membrane protein	Prion Protein (previously identified variant)	3 of 9	20p12.1-13	Metabolic/endocrine/cardiovascular	CNS Disorders	CNS Disorders	
29, 30 95124747	304	Agtccatcaatggac atggccatggaaatcat gttttttttttttttttt gggggggggggggggg aaccaggaggaggagg gttttttttttttttttt	A (29)	C (30)	Lys	Glu	NON-CONSERVATIVE	Calpastatin		184 of 150	17	Metabolic/endocrine/cardiovascular	

TABLE 1. *Estimated* *annual* *water* *use* *in* *the* *United* *States* *and* *Canada* *in* *1950* *and* *1951*

TABLE I
Effect of H_2O_2 on the Polymerization of $\text{CH}_2=\text{CH}-\text{CH}_2\text{Cl}$

TABLE I

TABLE 1: Summary of SNPs identified in the CuraGen dataset.

SEQ ID	Sequence Calling Assembly	Base pos. of SNP	Base of Polymorphic Sequence	Base before	Base after	Amino Acid before	Amino Acid after	Type of Change	Protein classification of CuraGen gene kinase	Name of protein identified following a BLASTX analysis of the CuraGen sequence	p value	Allele Freq. (pred.)	Map Location	Therapeutic Area #1	Therapeutic Area #2
61, 62	cg42709360	955	GGCGGGGA/GTG	C (61)	T (62)			Silent-Coding		Human Gene Similar to SWISS-PROT ID P17709 GLUCOKINASE (EC 2.7.1.2) (GLUCOSE KINASE) (GLK) - SACCHAROMYCES CEREVISIAE (BAKERS YEAST), 500 aa [pos SWISSPROT-ID P17709 GLUCOKINASE (EC 2.7.1.2) (GLUCOSE KINASE) (GLK) - SACCHAROMYCES CEREVISIAE (BAKERS YEAST), 500 aa]	4.10E-39		5 (Sq35.2)	Metabolic/endocrine/cardiovascular	
63, 64	cg43920091	21	GGGCCCTAGGTT	G (63)	gap (64)			SILENT-NONCODING	ATPase_associated	Human Gene SWISSPROT-ID Q13608 PEROXISOME ASSEMBLY FACTOR-2 (PAP-2) (PEROXISOMAL-TYPE ATPASE 1) (PEROXIN-6) - HOMO SAPIENS (HUMAN), 980 aa	0		6 (Sp21.1)	Metabolic/endocrine/cardiovascular	
65, 66	cg44913012	75	GGAGCTATAGGC	AATT (65)	gap (66)			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID Q01813 60 PHOSPHOFRUCTOKINASE, TYPE C (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTO-1-KINASE ISOZYME C) (6- PHOSPHOFRUCTOKINASE, PLATELET TYPE) - HOMO SAPIENS (HUMAN), 784 aa	40p deletion, 8 of 60		10 (10p15.3)	Metabolic/endocrine/cardiovascular	
67, 68	cg44913012	142	ATGAGACACA-	A (67)	G (68)			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID Q01813 60 PHOSPHOFRUCTOKINASE, TYPE C (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTO-1-KINASE ISOZYME C) (6- PHOSPHOFRUCTOKINASE, PLATELET TYPE) - HOMO SAPIENS (HUMAN), 784 aa	27 at75		10 (10p15.3)	Metabolic/endocrine/cardiovascular	

TABLE 1: Variants with significant association with the outcome of the study

SEQ ID	Sequence Calling Assembly	Base pos. of SNP	Base of Polymorphic Sequence	Base before	Base after	Amino Acid before	Amino Acid after	Type of Change	Protein classification of Curate gene	Name of protein identified following a BLASTX analysis of the Curate sequence	p value	Allele Freq. (pred.)	Map Location	Therapeutic Area #1	Therapeutic Area #2	
69,70	cg44913012	134	ATCTGAAAGC-ATGAGACACA-CTCC-ACAGACAGCAC[G (69)	A (70)			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID Q01813 6.0 (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE, TYPE C (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTOKINASE 1) (PHOSPHOFRUCTOKINASE-1-KINASE ISOZYME C) (6- PHOSPHOFRUCTOKINASE, PLATELET TYPE) - HOMO SAPIENS (HUMAN), 784 aa	15 of 75	10 (10p15.3)	Metabolic/endocrine/cardiovascular			
71,72	cg44913012	1530	CTGTC-AG-CC-G G (71) A-TTT-CTT- GATCT-GGCCCTT-GG-C-[A/G]AAGCC-G-T-CA-A-GCCAT-CA-TAGATGG-CG-AG-CAT-CCTG	T (72)				SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID Q01813 6.0 (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE, TYPE C (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTOKINASE 1) (PHOSPHOFRUCTOKINASE-1-KINASE ISOZYME C) (6- PHOSPHOFRUCTOKINASE, PLATELET TYPE) - HOMO SAPIENS (HUMAN), 784 aa	36 of 200	10 (10p15.3)	Metabolic/endocrine/cardiovascular			
73,74	cg44913012	1630	TGGCCGTGGCA G (73) AT-GCC-ACGG-C-A-CAG-G-CTGAGC-G-T-ACGGCTTCGGTT-CA-TCC-CA-GC-CGGGTGCC-C-ACGTTATGA	T (74)				SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID Q01813 6.0 (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE, TYPE C (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTOKINASE 1) (PHOSPHOFRUCTOKINASE-1-KINASE ISOZYME C) (6- PHOSPHOFRUCTOKINASE, PLATELET TYPE) - HOMO SAPIENS (HUMAN), 784 aa	35 of 200	10 (10p15.3)	Metabolic/endocrine/cardiovascular			
75,76	94238747	1638	TCT-CCGGGCCAACGTGATGGTGA-GGGGT-[T (75)	C (76)			SILENT-NONCODING		CD98		41 of 50	16q24.3	Metabolic/endocrine/cardiovascular	Immunology	

TABLE 1: SNPs with significant effect on protein expression

SEQ ID	Sequence Calling Assembly	Base pos. of SNP	Base Polymorphic	Base before	Base after	Amino Acid	Amino Acid after	Type of Change	Protein classification of Curate gene	Name of protein identified following a BLASTX analysis of the Curate gene sequence	p value	Allele Freq. (pred.)	Map Location	Therapeutic Area #1	Therapeutic Area #2	Renal Disease	
77, 78	95072341	286	TTTATAACAATAC	A (77)	gap (78)			NON-CODING	Kinase	sgk		46 of 200	5	Metabolic/endocrine/cardiovascular	Metabolic/endocrine/cardiovascular		
79, 80	95308656	445	AAAGGTGTGGAT	C (79)	T (80)	Gln		STOP	Termination	hpcortin 1	1.60E-07	2 of 150	9	Metabolic/endocrine/cardiovascular	Metabolic/endocrine/cardiovascular		
81, 82	cg43064060	805	AGAAACAA-	gap (81)	GTAG				Frameshift	nucl_recept			4.10E-254	4p insertion polymorphism 3 of 10	22	Metabolic/endocrine/cardiovascular	
83, 84	cg106711057	775	CGAT-GG-CT-T-	T (83)	A (84)	Lys	Asn	NON-CONSERVATIVE	Peptide hormone			2 of 130	6q13-15	Metabolic/endocrine/cardiovascular	CNS Disorders		

SEQ ID	Sequence Calling Assembly	Base pos. of SNP	Base of Polymorphic Sequence	Base before	Base after	Amino Acid before	Amino Acid after	Type of Change	Protein classification of CuratGen gene	Names of protein identified following a BLASTX analysis of the CuratGen sequence	p value	Allele Freq. (pred.)	Map Location	Therapeutic Area #1	Therapeutic Area #2
85, 86	cg106711057	477	/AAGKICATATGTC-C-TC-AG-TT ¹ AGG-CACAGJAA-CC-AAAATCCAG-TCTCT-CATATCCCGC[G/T]ATTTTTCCTTAAGCCTCTACTTGTGTTGATGTAAG	C (85)	T (86)	Tyr	Cys	NON-CONSERVATIVE	Peptide hormone	Acyl CoA Binding Protein	3 of 180	6q3.15	Metabolic/endocrinology/cardiovascular	CNS Disorders	
87, 88	cg108881866	170	TTCAGCT-GCACAG (87) TGAATAGAACAG (88) Met Ile	A (87)	A (88)	Met	Ile	Conservative	Peptide hormone	DBI-related Protein	10 of 60	6p24.1-25.3	Metabolic/endocrinology/cardiovascular	Oncology	
89, 90	cg108881866	741	G-CTGCC-AG-C-AA-GG-ATG-A-CITCAAT-CATCACTG-TTTAAC-AGG-AA-A-TGGTGA-CCTAGI-TF-ACA-G-TA-G-T-G-GGAA-TGA-T-CTG-A-CTAAC-T-T-C-AC-TG-ATA-T-T-CC-CC-C-T-G-C-T-G-AG-GAG	A (89)	G (90)	Cys	Tyr	NON-CONSERVATIVE	Peptide hormone	DBI-related Protein	3 of 200	6p24.1-25.3	Metabolic/endocrinology/cardiovascular	Oncology	

TABLE 1
SNPs with putative functional effects in the CuratCen gene

SEQ ID	Sequence Calling Assembly	Base pos. of SNP	Base pos. of Polymorphic Sequence	Base before	Base after	Amino Acid before	Amino Acid after	Type of Change	Protein classification of CuratCen gene	Name of protein identified following a BLASTX analysis of the CuratCen sequence	p value	Allele Freq. (pred.)	Map Location	Therapeutic Area #1	Therapeutic Area #2
91, 92	cg108881866	851	ATA- T -CC-CC-C- T - T-G-GT-GG-AG-T- AG-AG-GAG- AAAG-CTA- AAAATA(A/G)TG- CC-GT-ITTA-C- TGAGGGAA-T-TT- G-T- GGGGCTGTTTAT AGATTTT	A (91)	G (92)	Asn	Ser	NON-CONSERVATIVE	Peptide hormone	DBI-related Protein	3 of 200	6p24.1-25.3	Metabolic/endocrine/ cardiovascular	Oncology	
93, 94	cg108881866	1309	C-AC-TTTT-C-AG- AAAAGAAG- TCTGGAA- CCAGGC-T-GAA- GGCA-TTTGC- AAAGCTT- CCCCC-AAAT- GIC/T] CTTG-AG- AATT-C-AAAAG- AGG-TAAT-CA- GG-AAAAG- AGAGAG-A-G- AAAAACTACAC- GCT-GT-T-AATG-C TGA-AGAGATG- CAAT-G-T-CC- TTCAAG	C (93)	T (94)	Val	Ala	Conservative	Peptide hormone	DBI-related Protein	8 of 50	6p24.1-25.3	Metabolic/endocrine/ cardiovascular	Oncology	

TABLE I
Comparison of the Results of the Determination of the Mg^{2+} Content in the Water by the Ion-Selective Electrode Method and by the Spectrophotometric Method

Sequence Calling Assembly	Base pos. of SNP	Base pos. of Polymorphic Sequence	Amino Acid before	Amino Acid after	Type of Change	Protein classification of Curagen gene	Name of protein identified following a BLASTX analysis of the Curagen sequence	p value	Allele freq. (pred.)	Map Location	Therapeutic Area	
											#1	#2
cg1088818655_96	1404	AAATT-CAAAAG-T(95)	G(96)	Cys	Trp	NON-CONSERVATIVE	DBI-related Protein	6p24.1-25.3	2 of 40	Metabolic/endocrinologic/cardiovascular	Oncology	